

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10781, 060  
Source: IFW0  
Date Processed by STIC: 2-2-05

***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 02/02/2005

PATENT APPLICATION: US/10/781,060

TIME: 16:15:30

Input Set : E:\7326-131 SEQLIST.TXT

Output Set: N:\CRF4\02022005\J781060.raw

4 <110> APPLICANT: Artavanis-Tsakonas, Spyridon,  
 5 Fehon, Richard Grant  
 6 Zagouras, Panayiotis  
 7 Blaumueller, Christine Marie  
 9 <120> TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND  
 10 COMPOSITIONS BASED ON NOTCH PROTEINS AND NUCLEIC ACIDS  
 13 <130> FILE REFERENCE: 7326-131-999  
 15 <140> CURRENT APPLICATION NUMBER: 10/781,060  
 16 <141> CURRENT FILING DATE: 2004-02-17  
 18 <150> PRIOR APPLICATION NUMBER: 09/564,504  
 19 <151> PRIOR FILING DATE: 2000-05-04  
 21 <150> PRIOR APPLICATION NUMBER: 08/532,384  
 22 <151> PRIOR FILING DATE: 1995-09-22  
 24 <150> PRIOR APPLICATION NUMBER: 08/083,590  
 25 <151> PRIOR FILING DATE: 1993-06-25  
 27 <150> PRIOR APPLICATION NUMBER: 07/955,012  
 28 <151> PRIOR FILING DATE: 1992-09-30  
 30 <150> PRIOR APPLICATION NUMBER: 07/879,038  
 31 <151> PRIOR FILING DATE: 1992-04-30  
 33 <160> NUMBER OF SEQ ID NOS: 21  
 35 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 37 <210> SEQ ID NO: 1  
 38 <211> LENGTH: 2892  
 39 <212> TYPE: DNA  
 40 <213> ORGANISM: Drosophila  
 42 <220> FEATURE:  
 43 <221> NAME/KEY: CDS  
 44 <222> LOCATION: (142)...(2640)  
 45 <223> OTHER INFORMATION: Drosophila Delta cDNA (C11)  
 47 <400> SEQUENCE: 1  
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 49 cacacacaca cacagcccgt ggattattac actaaaagcg acactcaatc caaaaaatca 120  
 50 gcaacaaaaa catcaataaa c atg cat tgg att aaa tgt tta tta aca gca 171  
 51 Met His Trp Ile Lys Cys Leu Leu Thr Ala  
 52 1 5 10  
 54 ttc att tgc ttc aca gtc atc gtg cag gtt cac agt tcc ggc agc ttt 219  
 55 Phe Ile Cys Phe Thr Val Ile Val Gln Val His Ser Ser Gly Ser Phe  
 56 15 20 25  
 58 gag ttg cgc ctg aag tac ttc agc aac gat cac ggg cgg gac aac gag 267  
 59 Glu Leu Arg Leu Lys Tyr Phe Ser Asn Asp His Gly Arg Asp Asn Glu  
 60 30 35 40  
 62 ggt cgc tgc tgc agc ggg gag tcg gac gga gcg acg ggc aag tgc ctg 315  
 63 Gly Arg Cys Cys Ser Gly Glu Ser Asp Gly Ala Thr Gly Lys Cys Leu

(pg. 6)

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64	45	50	55	
66 ggc agc tgc aag acg cgg ttt cgc gtc tgc cta aag cac tac cag gcc	363			
67 Gly Ser Cys Lys Thr Arg Phe Arg Val Cys Leu Lys His Tyr Gln Ala				
68 60 65 70				
70 acc atc gac acc acc tcc cag tgc acc tac ggg gac gtg atc acg ccc	411			
71 Thr Ile Asp Thr Thr Ser Gln Cys Thr Tyr Gly Asp Val Ile Thr Pro				
72 75 80 85 90				
74 att ctc ggc gag aac tcg gtc aat ctg acc gac gcc cag cgc ttc cag	459			
75 Ile Leu Gly Glu Asn Ser Val Asn Leu Thr Asp Ala Gln Arg Phe Gln				
76 95 100 105				
78 aac aag ggc ttc acg aat ccc atc cag ttc ccc ttc tcg ttc tca tgg	507			
79 Asn Lys Gly Phe Thr Asn Pro Ile Gln Phe Pro Phe Ser Phe Ser Trp				
80 110 115 120				
82 ccg ggt acc ttc tcg ctg atc gtc gag gcc tgg cat gat acg aac aat	555			
83 Pro Gly Thr Phe Ser Leu Ile Val Glu Ala Trp His Asp Thr Asn Asn				
84 125 130 135				
86 agc ggc aat gcg cga acc aac aag ctc ctc atc cag cga ctc ttg gtg	603			
87 Ser Gly Asn Ala Arg Thr Asn Lys Leu Leu Ile Gln Arg Leu Leu Val				
88 140 145 150				
90 cag cag gta ctg gag gtg tcc tcc gaa tgg aag acg aac aag tcg gaa	651			
91 Gln Gln Val Leu Glu Val Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu				
92 155 160 165 170				
94 tcg cag tac acg tcg ctg gag tac gat ttc cgt gtc acc tgc gat ctc	699			
95 Ser Gln Tyr Thr Ser Leu Glu Tyr Asp Phe Arg Val Thr Cys Asp Leu				
96 175 180 185				
98 aac tac tac gga tcc ggc tgt gcc aag ttc tgc cgg ccc cgc gac gat	747			
99 Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys Arg Pro Arg Asp Asp				
100 190 195 200				
102 tca ttt gga cac tcg act tgc tcg gag acg ggc gaa att atc tgt ttg	795			
103 Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu				
104 205 210 215				
106 acc gga tgg cag ggc gat tac tgt cac ata ccc aaa tgc gcc aaa ggc	843			
107 Thr Gly Trp Gln Gly Asp Tyr Cys His Ile Pro Lys Cys Ala Lys Gly				
108 220 225 230				
110 tgt gaa cat gga cat tgc gac aaa ccc aat caa tgc gtt tgc caa ctg	891			
111 Cys Glu His Gly His Cys Asp Lys Pro Asn Gln Cys Val Cys Gln Leu				
112 235 240 245 250				
114 ggc tgg aag gga gcc ttg tgc aac gag tgc gtt ctg gaa ccg aac tgc	939			
115 Gly Trp Lys Gly Ala Leu Cys Asn Glu Cys Val Leu Glu Pro Asn Cys				
116 255 260 265				
118 atc cat ggc acc tgc aac aaa ccc tgg act tgc atc tgc aac gag ggt	987			
119 Ile His Gly Thr Cys Asn Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly				
120 270 275 280				
122 tgg gga ggc ttg tac tgc aac cag gat ctg aac tac tgc acc aac cac	1035			
123 Trp Gly Gly Leu Tyr Cys Asn Gln Asp Leu Asn Tyr Cys Thr Asn His				
124 285 290 295				
126 aga ccc tgc aag aat ggc gga acc tgc ttc aac acc ggc gag gga ttg	1083			
127 Arg Pro Cys Lys Asn Gly Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu				
128 300 305 310				

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130	tac	aca	tgc	aaa	tgc	gct	cca	gga	tac	agt	ggt	gat	gat	tgc	gaa	aat	1131
131	Tyr	Thr	Cys	Lys	Cys	Ala	Pro	Gly	Tyr	Ser	Gly	Asp	Asp	Cys	Glu	Asn	
132	315					320					325					330	
134	gag	atc	tac	tcc	tgc	gat	gcc	gat	gtc	aat	ccc	tgc	cag	aat	ggt	ggt	1179
135	Glu	Ile	Tyr	Ser	Cys	Asp	Ala	Asp	Val	Asn	Pro	Cys	Gln	Asn	Gly	Gly	
136					335					340						345	
138	acc	tgc	atc	gat	gag	ccg	cac	aca	aaa	acc	ggc	tac	aag	tgt	cat	tgc	1227
139	Thr	Cys	Ile	Asp	Glu	Pro	His	Thr	Lys	Thr	Gly	Tyr	Lys	Cys	His	Cys	
140				350						355						360	
142	gcc	aac	ggc	tgg	agc	gga	aag	atg	tgc	gag	gag	aaa	gtg	ctc	acg	tgt	1275
143	Ala	Asn	Gly	Trp	Ser	Gly	Lys	Met	Cys	Glu	Glu	Lys	Val	Leu	Thr	Cys	
144			365					370					375				
146	tcg	gac	aaa	ccc	tgt	cat	cag	gga	atc	tgc	cgc	aac	gtt	cgt	cct	ggc	1323
147	Ser	Asp	Lys	Pro	Cys	His	Gln	Gly	Ile	Cys	Arg	Asn	Val	Arg	Pro	Gly	
148		380					385					390					
150	ttg	gga	agc	aag	ggt	cag	ggc	tac	cag	tgc	gaa	tgt	ccc	att	ggc	tac	1371
151	Leu	Gly	Ser	Lys	Gly	Gln	Gly	Tyr	Gln	Cys	Glu	Cys	Pro	Ile	Gly	Tyr	
152	395					400					405					410	
154	agc	gga	ccc	aac	tgc	gat	ctc	cag	ctg	gac	aac	tgc	agt	ccg	aat	cca	1419
155	Ser	Gly	Pro	Asn	Cys	Asp	Leu	Gln	Leu	Asp	Asn	Cys	Ser	Pro	Asn	Pro	
156				415						420						425	
158	tgc	ata	aac	ggt	gga	agc	tgt	cag	ccg	agc	gga	aag	tgt	att	tgc	cca	1467
159	Cys	Ile	Asn	Gly	Gly	Ser	Cys	Gln	Pro	Ser	Gly	Lys	Cys	Ile	Cys	Pro	
160			430					435						440			
162	gcg	gga	ttt	tcg	gga	acg	aga	tgc	gag	acc	aac	att	gac	gat	tgt	ctt	1515
163	Ala	Gly	Phe	Ser	Gly	Thr	Arg	Cys	Glu	Thr	Asn	Ile	Asp	Asp	Cys	Leu	
164			445					450					455				
166	ggc	cac	cag	tgc	gag	aac	gga	ggc	acc	tgc	ata	gat	atg	gtc	aac	caa	1563
167	Gly	His	Gln	Cys	Glu	Asn	Gly	Gly	Thr	Cys	Ile	Asp	Met	Val	Asn	Gln	
168		460					465					470					
170	tat	cgc	tgc	caa	tgc	gtt	ccc	ggt	ttc	cat	ggc	acc	cac	tgt	agt	agc	1611
171	Tyr	Arg	Cys	Gln	Cys	Val	Pro	Gly	Phe	His	Gly	Thr	His	Cys	Ser	Ser	
172	475					480					485					490	
174	aaa	gtt	gac	ttg	tgc	ctc	atc	aga	ccg	tgt	gcc	aat	gga	gga	acc	tgc	1659
175	Lys	Val	Asp	Leu	Cys	Leu	Ile	Arg	Pro	Cys	Ala	Asn	Gly	Gly	Thr	Cys	
176				495						500						505	
178	ttg	aat	ctc	aac	aac	gat	tac	cag	tgc	acc	tgt	cgt	gcg	gga	ttt	act	1707
179	Leu	Asn	Leu	Asn	Asp	Tyr	Gln	Cys	Thr	Cys	Arg	Ala	Gly	Phe	Thr		
180				510					515					520			
182	ggc	aag	gat	tgc	tct	gtg	gac	atc	gat	gag	tgc	agc	agt	gga	ccc	tgt	1755
183	Gly	Lys	Asp	Cys	Ser	Val	Asp	Ile	Asp	Glu	Cys	Ser	Ser	Gly	Pro	Cys	
184			525					530					535				
186	cat	aac	ggc	ggc	act	tgc	atg	aac	cgc	gtc	aat	tcg	ttc	gaa	tgc	gtg	1803
187	His	Asn	Gly	Gly	Thr	Cys	Met	Asn	Arg	Val	Asn	Ser	Phe	Glu	Cys	Val	
188		540					545					550					
190	tgt	gcc	aat	ggt	ttc	agg	ggc	aag	cag	tgc	gat	gag	gag	tcc	tac	gat	1851
191	Cys	Ala	Asn	Gly	Phe	Arg	Gly	Lys	Gln	Cys	Asp	Glu	Glu	Ser	Tyr	Asp	
192	555					560					565					570	
194	tcg	gtg	acc	ttc	gat	gcc	cac	caa	tat	gga	gcg	acc	aca	caa	gcg	aga	1899

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195	Ser	Val	Thr	Phe	Asp	Ala	His	Gln	Tyr	Gly	Ala	Thr	Thr	Gln	Ala	Arg	
196					575					580					585		
198	gcc	gat	ggt	ttg	acc	aat	gcc	cag	gta	gtc	cta	att	gct	gtt	ttc	tcc	1947
199	Ala	Asp	Gly	Leu	Thr	Asn	Ala	Gln	Val	Val	Leu	Ile	Ala	Val	Phe	Ser	
200					590					595					600		
202	gtt	gcg	atg	cct	ttg	gtg	gcg	gtt	att	gcg	gcg	tgc	gtg	gtc	ttc	tgc	1995
203	Val	Ala	Met	Pro	Leu	Val	Ala	Val	Ile	Ala	Ala	Cys	Val	Val	Phe	Cys	
204					605					610					615		
206	atg	aag	cgc	aag	cgt	aag	cgt	gct	cag	gaa	aag	gac	gac	gcg	gag	gcc	2043
207	Met	Lys	Arg	Lys	Arg	Lys	Arg	Ala	Gln	Glu	Lys	Asp	Asp	Ala	Glu	Ala	
208					620					625					630		
210	agg	aag	cag	aac	gaa	cag	aat	gcg	gtg	gcc	aca	atg	cat	cac	aat	ggc	2091
211	Arg	Lys	Gln	Asn	Glu	Gln	Asn	Ala	Val	Ala	Thr	Met	His	His	Asn	Gly	
212	635									640					645		650
214	agt	ggg	gtg	ggt	gta	gct	ttg	gct	tca	gcc	tct	ctg	ggc	ggc	aaa	act	2139
215	Ser	Gly	Val	Gly	Val	Ala	Leu	Ala	Ser	Ala	Ser	Leu	Gly	Gly	Lys	Thr	
216					655					660					665		
218	ggc	agc	aac	agc	ggt	ctc	acc	ttc	gat	ggc	ggc	aac	ccg	aat	atc	atc	2187
219	Gly	Ser	Asn	Ser	Gly	Leu	Thr	Phe	Asp	Gly	Gly	Asn	Pro	Asn	Ile	Ile	
220					670					675					680		
222	aaa	aac	acc	tgg	gac	aag	tcg	gtc	aac	aac	att	tgt	gcc	tca	gca	gca	2235
223	Lys	Asn	Thr	Trp	Asp	Lys	Ser	Val	Asn	Asn	Ile	Cys	Ala	Ser	Ala	Ala	
224					685					690					695		
226	gca	gcg	gcg	gcg	gcg	gca	gca	gcg	gcg	gac	gag	tgt	ctc	atg	tac	ggc	2283
227	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Asp	Glu	Cys	Leu	Met	Tyr	
228					700					705					710		
230	gga	tat	gtg	gcc	tcg	gtg	gcg	gat	aac	aac	aat	gcc	aac	tca	gac	ttt	2331
231	Gly	Tyr	Val	Ala	Ser	Val	Ala	Asp	Asn	Asn	Asn	Ala	Asn	Ser	Asp	Phe	
232	715									720					725		730
234	tgt	gtg	gct	ccg	cta	caa	aga	gcc	aag	tcg	caa	aag	caa	ctc	aac	acc	2379
235	Cys	Val	Ala	Pro	Leu	Gln	Arg	Ala	Lys	Ser	Gln	Lys	Gln	Leu	Asn	Thr	
236					735					740					745		
238	gat	ccc	acg	ctc	atg	cac	cg	ggt	tcg	ccg	gca	ggc	agc	tca	gcc	aag	2427
239	Asp	Pro	Thr	Leu	Met	His	Arg	Gly	Ser	Pro	Ala	Gly	Ser	Ser	Ala	Lys	
240					750					755					760		
242	gga	gcg	tct	ggc	gga	gga	ccg	gga	gcg	gcg	gag	ggc	aag	agg	atc	tct	2475
243	Gly	Ala	Ser	Gly	Gly	Gly	Pro	Gly	Ala	Ala	Glu	Gly	Lys	Arg	Ile	Ser	
244					765					770					775		
246	gtt	tta	ggc	gag	ggt	tcc	tac	tgt	agc	cag	cg	tgg	ccc	tcg	ttg	gcg	2523
247	Val	Leu	Gly	Glu	Gly	Ser	Tyr	Cys	Ser	Gln	Arg	Trp	Pro	Ser	Leu	Ala	
248					780					785					790		
250	gcg	gcg	gga	gtg	gcc	gga	gcc	tgt	tca	tcc	cag	cta	atg	gct	gca	gct	2571
251	Ala	Ala	Gly	Val	Ala	Gly	Ala	Cys	Ser	Ser	Gln	Leu	Met	Ala	Ala	Ala	
252	795									800					805		810
254	tcg	gca	gcg	ggc	agc	gga	gcg	ggg	acg	gcg	caa	cag	cag	cga	tcc	gtg	2619
255	Ser	Ala	Ala	Gly	Ser	Gly	Ala	Gly	Thr	Ala	Gln	Gln	Gln	Arg	Ser	Val	
256					815					820					825		
258	gtc	tgc	ggc	act	ccg	cat	atg	taactccaaa	aatccggaag	ggctcctggt							2670
259	Val	Cys	Gly	Thr	Pro	His	Met										

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260          830
262 aaatccggag aaatccgcat ggaggagctg acagcacata cacaaagaaa agactggggt 2730
263 ggggttcaaaa tgtgagagag acgcaaaaat gttgttggtg attgaagcag tttagtcgtc 2790
264 acgaaaaaatg aaaaatctgt aacaggcata actcgtaaac tccctaaaaa atttgtatag 2850
265 taattagcaa agctgtgacc cagccgtttc gatcccgaaat tc 2892
267 <210> SEQ ID NO: 2
268 <211> LENGTH: 833
269 <212> TYPE: PRT
270 <213> ORGANISM: Drosophila
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Drosophila Delta protein (C11)
275 <400> SEQUENCE: 2
276 Met His Trp Ile Lys Cys Leu Leu Thr Ala Phe Ile Cys Phe Thr Val
277 1 5 10 15
278 Ile Val Gln Val His Ser Ser Gly Ser Phe Glu Leu Arg Leu Lys Tyr
279 20 25 30
280 Phe Ser Asn Asp His Gly Arg Asp Asn Glu Gly Arg Cys Cys Ser Gly
281 35 40 45
282 Glu Ser Asp Gly Ala Thr Gly Lys Cys Leu Gly Ser Cys Lys Thr Arg
283 50 55 60
284 Phe Arg Val Cys Leu Lys His Tyr Gln Ala Thr Ile Asp Thr Thr Ser
285 65 70 75 80
286 Gln Cys Thr Tyr Gly Asp Val Ile Thr Pro Ile Leu Gly Glu Asn Ser
287 85 90 95
288 Val Asn Leu Thr Asp Ala Gln Arg Phe Gln Asn Lys Gly Phe Thr Asn
289 100 105 110
290 Pro Ile Gln Phe Pro Phe Ser Phe Ser Trp Pro Gly Thr Phe Ser Leu
291 115 120 125
292 Ile Val Glu Ala Trp His Asp Thr Asn Asn Ser Gly Asn Ala Arg Thr
293 130 135 140
294 Asn Lys Leu Leu Ile Gln Arg Leu Leu Val Gln Gln Val Leu Glu Val
295 145 150 155 160
296 Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu Ser Gln Tyr Thr Ser Leu
297 165 170 175
298 Glu Tyr Asp Phe Arg Val Thr Cys Asp Leu Asn Tyr Tyr Gly Ser Gly
299 180 185 190
300 Cys Ala Lys Phe Cys Arg Pro Arg Asp Asp Ser Phe Gly His Ser Thr
301 195 200 205
302 Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu Thr Gly Trp Gln Gly Asp
303 210 215 220
304 Tyr Cys His Ile Pro Lys Cys Ala Lys Gly Cys Glu His Gly His Cys
305 225 230 235 240
306 Asp Lys Pro Asn Gln Cys Val Cys Gln Leu Gly Trp Lys Gly Ala Leu
307 245 250 255
308 Cys Asn Glu Cys Val Leu Glu Pro Asn Cys Ile His Gly Thr Cys Asn
309 260 265 270
310 Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly Trp Gly Gly Leu Tyr Cys
311 275 280 285
312 Asn Gln Asp Leu Asn Tyr Cys Thr Asn His Arg Pro Cys Lys Asn Gly

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; N Pos. 399

Seq#:9; N Pos. 38,39,263,264,265,283,285,306

**VERIFICATION SUMMARY**

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L:563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:360

L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0

M:341 Repeated in SeqNo=9